

GeneCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 1, 2002, 05:37:35 ; Search time 5265 seconds
(without alignments)
16995.607 Million cell updates/sec

Title: US-09-730-559B-1

Perfect score:

1 ttcttacgtttttccctgc.....atcagaaaaaaaaaaaaa 4276

Scoring table:

IDENTITY_NUC

GapOp 10.0 , Gapext 1.0

Searched:

1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters:

3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

General:*

1: gb-ba:*

2: gb-hgtg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_rdat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_r01:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pa:*

24: em_ph:*

25: em_pl:*

26: em_r01:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hgtg_hum:*

31: em_hgtg_inv:*

32: em_hgtg_other:*

33: em_hgtg_inv:*

RESULT 1
AC023404
LOCUS AC023404 DNA lineal HTG 01-MAR-2000
DEFINITION Homo sapiens clone RP11-619L12, WORKING DRAFT SEQUENCE, 10
unordered pieces.
ACCESSION AC023404
VERSION AC023404.2 GI:7139760
KEYWORDS HTG; HTGS-PHASE1; HTGS_DRAFT.
SOURCE Human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Gatarhini; Homindae; Homo.
Mammalia; Eutheria; Primates; Gatarhini; Homindae; Homo.
1 (bases 1 to 167659)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	Score	Query	Match	Length	DB	ID	Description
1	103054	CHS01PA	2	135038	9	AC01193	Homo sapiens
2	181740	CHS01PA	2	135038	9	AC01193	Homo sapiens
3	113687	CHS01PA	2	135038	9	AC01193	Homo sapiens
4	113687	CHS01PA	2	135038	9	AC01193	Homo sapiens
5	155691	CHS01PA	2	135038	9	AC01193	Homo sapiens
6	167988	CHS01PA	2	135038	9	AC01193	Homo sapiens
7	181532	CHS01PA	2	135038	9	AC01193	Homo sapiens
8	187696	CHS01PA	2	135038	9	AC01193	Homo sapiens
9	214872	CHS01PA	2	135038	9	AC01193	Homo sapiens
10	22094	CHS01PA	2	135038	9	AC01193	Homo sapiens
11	2294	CHS01PA	2	135038	9	AC01193	Homo sapiens
12	2314	CHS01PA	2	135038	9	AC01193	Homo sapiens
13	2331	CHS01PA	2	135038	9	AC01193	Homo sapiens
14	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
15	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
16	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
17	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
18	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
19	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
20	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
21	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
22	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
23	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
24	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
25	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
26	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
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28	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
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30	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
31	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
32	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
33	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
34	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
35	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
36	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
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39	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
40	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
41	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
42	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
43	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
44	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens
45	2340	CHS01PA	2	135038	9	AC01193	Homo sapiens

SUMMARIES

Anderson, S., Baldwin, J., Beda, F., Bousliskiy, L.,
Bouklal, B., Brown, J., Campopiano, A., Castle, A.,
Choevel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Dearellan, K., Dearan, K., Dodge, S., Domino, M., Doyle, M.,
Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D.,
Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Db	19182	TTTGCTCCCTCTTTCATCCCTTTTACGATGGAGGAGTA	19241
QY	4129	acatattttaaatggaaagacatgttagccaaacaaatgcataaagactatgcgc	4188
Db	19242	ACATTTTAACTGGAAAGAGGAGCTAGCCAACTAGCTTACGAGACTGAC	19301
QY	4189	atataatattttatcggttttaggtgacatattttatccctccaaaaatgt	4248
Db	19302	ATTAATAATTTCTCGGTTAGGCTGACATAATTCTCAATACCTCAAAAGT	19361
QY	4249	acccacatcgaaaaaaaataaaaa 4276	
Db	19362	ACACCAACATCAGAAAAATTAANAA 19389	
	RESULT	4	
AC027609/C	AC027609	157320 bp DNA linear HTG 01-SEP-2000	
LOCUS	Homo sapiens chromosome 5 clone RP11-80E21, WORKING DRAFT SEQUENCE,		
DEFINITION	34 unorderd pieces.		
ACCESSION	AC027609		
VERSION	AC027609_3		
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.		
SOURCE			
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
	-----	Genome Center	-----
	Center: Washington University Genome Sequencing Center		
	Center code: WUGSC		
	Waterston, R.H.		
	The sequence of Homo sapiens		
	Unpublished		
	2 (bases 1 to 157320)		
	Waterston, R.H.		
	Direct Submission		
	Submitted (30-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 444 Forest Park Parkway, St. Louis, MO 63108, USA		
	On Sep 1, 2000 this sequence version replaced 91:7637328.		

	Sequencing vector: M13; 100%		
	Sequencing vector: Plasmid; 0%		
	Chemistry: Dye-Primer; 100% of reads		
	Chemistry: Dye-Primer; ET; 100% of reads		
	Assembly program: Phrap; version 0.990319		
	Consensus quality: 138437 bases at least 040		
	Consensus quality: 146655 bases at least 030		
	Consensus quality: 14934 bases at least 020		
	Insert size: 167000; agarose-fp		
	Insert size: 153159; sum-of-contigs		
	Quality coverage: 3.44 in 020 bases; agarose-fp		
	Quality coverage: 3.89 in 020 bases; sum-of-contigs		

	* NOTE: this is a "working draft" sequence. It currently		
	* consists of 34 contigs. The true order of the pieces		
	* is not known and their order in this sequence record is		
	* arbitrary. Gaps between the contigs are represented as		
	* runs of N, but the exact sizes of the gaps are unknown.		
	* This record will be updated with the finished sequence		
	* as soon as it is available and the accession number will		
	* be preserved.		
	1. 1657: contig of 1657 bp in length		
	1658 177: gap of unknown length		
	1758 344: contig of 1697 bp in length		
	3455 355: gap of unknown length		
	3555 3556: contig of 1582 bp in length		

	FEATURES		
	source		
	/organism="Homo sapiens"		
	/chromosome="5"		
	/clone="RP11-80E21"		
	1. 1657		
	/note="Assembly_name:contig14"		
	1758 3454		
	/note="Assembly_name:contig15"		
	3555 3556		

